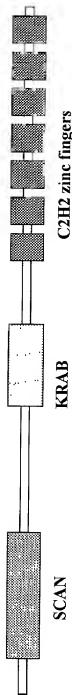


Structure of MDZ3 and alignment of SCAN box and KRAB motifs

A

MDZ3 (544 a.a.)



B

SCAN box

consensus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
MDZ3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 11136033	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 6226799	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 3046745	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 3006231	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 1731420	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 11136100	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
gi 2978255	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60

consensus	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252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KRAB motif

	10	20	30	40	50	60
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consensus	1	VTFFDVAVYFSQEEWEQLDPAQKNLYRDVM-	LENYSNLVSLG-FKVPKP----	DLISQL	53	
MDZ3	230	gpFKDMALAFPEEWRHVTPAQIDCFGEYVpQDCR--	VSPG-GGSKK-----	BAKPPQ	281	
gi 1061424	104	VSKFDVAVFTQEEWRQLDPDEKTAYGDVM-	LENYSHLVSVG-YDYHQAkhhgVEVKEV	161		
gi 1731409	1	MAFRDVAVFTQDEWRLLSPAORTLYREVVM-	LENYSNLVSLG-ISFSKP-----	ELITQL	53	
gi 2887445	14	VTFFDVAVFTKEEWGQLDLAORTLYREVVT-	LETWEHIVSLG1-FLSKS-----	DVISQL	66	
gi 7636871	14	VCFFDVAVFTQEEWEQLDLAORTLYREVVT-	LETWEHIVSLG1-FLSKS-----	DVISQL	66	
gi 2507555	8	VTFFDVAVFTSEELQLDLAQRKLYRDVM-	LENFRNVSVGhQSTP-----	DGLPOL	59	
gi 11136087	3	LTFKDVAVFTSEELGLLDLPVQRNLYQDVM-	LENFRNLLSVGhHPFK-----	HDVFLI	54	
******					
consensus	54	EQGEEPWI	61			
MDZ3	282	EDLkgalv	289			
gi 1061424	162	EQGEEPWI	169			
gi 1731409	54	EQKETWR	61			
gi 2887445	67	EHGQEPWT	74			
gi 7656871	67	EQEEDLCR	74			
gi 2507555	60	EREKLWM	67			
gi 11136087	55	EKEKLDI	62			

FIG. 1

102080"18122663

MDZ3 gene (chr. 7q22.1)

AC005020 (177,531 bp) (MDZ3 locus spans 14 kb)

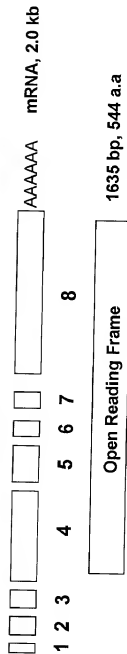


FIG. 2

MDZ3

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

1 c gga tag cac tgg cga ccc tag cgg gtg aga ggc cct
 38 tca ggg cgg cgg cgg gtt gag cgc acc atc aca tct aag
 77 cca tca gca agt ttg ttg gtt tta atc tcc aaa ata cgt
 116 ctt gat ttt gtc tga ctc ttt gcc acc acc ctg atc taa
 155 gcc ctt atc atc tgc ttg aat cac taa ctt gtc tcc act
 194 tgc agt ttt taa aag agt tgc ttc cat ttg act ttt tct
 233 gtc tgc tgt acc aac ata tga gtt tca gga ggg gtc att
 272 gat gca gtc att ctc agt ctc ctc gga ggg agt ctg aag
 311 M L K E H P E M A E A P Q
 ATG CTT AAA GAG CAT CCA GAG ATG GCG GAA GCT CCT CAG
 350 Q Q L G I P V V K L E K E
 CAG CAG TTG GGT ATT CCT GTG GTG AAA CTG GAG AAA GAG
 389 L P W G R G R E D P S P E
 TTG CCA TGG GGC AGA GGA AGG GAG GAC CCT AGT CCA GAG
 428 T F R L R F R Q F R Y Q E
 ACT TTT CGG CTG AGG TTT CGG CAG TTC CGC TAC CAG GAG
 467 A A G P Q E A L R G G L Q E
 GCA GCT GGA CCC CAG GAA GCT CTT AGG GGC CTC CAG GAG
 506 L C R R W L R P E L H T K
 CTC TGT CGT CGG TGG CTG AGG CCC GAG TTG CAC ACC AAG
 545 E Q I L E L L V L E Q F L
 GAG CAG ATC CTG GAG CTG CTG GTG CTG GAG CAG TTC CTC
 584 T I L P R E F Y A W I R E
 ACT ATC CTG CCC CGC GAG TTC TAC GCC TGG ATC CGG GAG
 623 H G P E S G K A L A A M V
 CAT GGC CCA GAG AGT GGC AAG GCC CTG GCC GCC ATG GTG

FIG. 3

E D L T E R A L E A K A V
 662 GAG GAC CTG ACA GAA AGA GCA CTG GAG GCC AAG GCG GTT

 P C H R Q G E Q E E T A L
 701 CCA TGC CAC AGG CAG GGA GAG CAG GAG GAA ACA GCA CTT

 C R G A W E P G I Q L G P
 740 TGC AGA GGC GCT TGG GAG CCA GGC ATC CAG CTG GGG CCA

 V E V K P E W G M P P G E
 779 GTG GAG GTT AAG CCT GAA TGG GGG ATG CCC CCT GGG GAA

 G V Q G P D P G T E E Q L
 818 GGA GTT CAA GGT CCA GAC CCA GGT ACC GAG GAG CAG CTC

 S Q D P G D E T R A F Q E
 857 AGT CAG GAC CCT GGA GAT GAG ACA CGG GCC TTC CAG GAG

 Q A L P V L Q A G P G L P
 896 CAA GCA CTA CCT GTT CTG CAG GCG GGT CCT GGC CTC CCC

 A V N P R D Q E M A A G F
 935 GCA GTG AAT CCC AGA GAC CAA GAG ATG GCA GCT GGG TTC

 F T A G S Q G L G P F K D
 974 TTT ACT GCT GGA TCG CAG GGG TTG GGG CCA TTT AAA GAT

 M A L A F P E E E W R H V
 1013 ATG GCC CTG GCC TTC CCT GAG GAG GAG TGG AGG CAT GTG

 T P A Q I D C F G E Y V E
 1052 ACC CCA GCC CAG ATA GAC TGC TTT GGG GAG TAT GTG GAA

 P Q D C R V S P G G S K
 1091 CCG CAG GAC TGC AGG GTC TCT CCA GGC GGT GGG AGC AAG

 E K E A K P P Q E D L K G
 1130 GAA AAG GAG GCA AAA CCC CCA CAG GAA GAC CTG AAA GGG

 A L V A L T S E R F G E A
 1169 GCG CTG GTG GCA CTG ACA TCA GAG AGG TTT GGG GAA GCC

 S L Q G P G L G R V C E Q
 1208 TCT CTC CAG GGC CCT GGG CTC GGA AGG GTC TGT GAG CAG

 E P G G P A G S A P G L P
 1247 GAG CCT GGT GGC CCT GCA GGC AGT GCG CCT GGG CTT CCT

FIG. 3

09922181.080201

	P	P	Q	H	G	A	I	P	L	P	D	E	V
1286	CCT	CCC	CAG	CAC	GGT	GCC	ATC	CCC	CTG	CCT	GAC	GAA	GTC
	K	T	H	S	S	F	W	K	P	F	Q	C	P
1325	AAA	ACC	CAC	AGC	TCC	TTC	TGG	AAG	CCT	TTC	CAG	TGC	CCT
	E	C	G	K	G	F	S	R	S	S	N	L	V
1364	GAG	TGT	GGG	AAA	GGA	TTC	AGT	CGG	AGC	TCC	AAT	CTC	GTC
	R	H	Q	R	T	H	E	E	K	S	Y	G	C
1403	AGG	CAC	CAG	CGA	ACC	CAC	GAA	GAG	AAG	TCT	TAT	GGC	TGT
	V	E	C	G	K	G	F	T	L	R	E	Y	L
1442	GTG	GAG	TGT	GGG	AAG	GGC	TTT	ACC	CTG	AGA	GAG	TAC	CTG
	M	K	H	Q	R	T	H	L	G	K	R	P	Y
1481	ATG	AAG	CAC	CAG	AGA	ACC	CAC	CTG	GGA	AAG	AGG	CCC	TAC
	V	C	S	E	C	W	K	T	F	S	Q	R	H
1520	GTG	TGC	AGC	GAG	TGC	TGG	AAA	ACC	TTC	AGC	CAG	AGA	CAC
	H	L	E	V	H	Q	R	S	H	T	G	E	K
1559	CAC	CTG	GAG	GTG	CAC	CAG	CGC	AGC	CAC	ACT	GGG	GAG	AAG
	P	H	K	C	G	D	C	W	K	S	F	S	R
1598	CCC	CAC	AAG	TGC	GGG	GAC	TGC	TGG	AAG	AGC	TTC	AGC	CGC
	R	Q	H	L	Q	V	H	R	R	T	H	T	G
1637	AGG	CAG	CAC	CTG	CAG	GTG	CAC	CGG	AGG	AGC	CAC	ACC	GGG
	E	K	P	Y	T	C	E	C	G	K	S	F	S
1676	GAG	AAG	CCC	TAC	ACC	TGC	GAG	TGT	GGC	AAG	AGC	TTC	AGC
	R	N	A	N	L	A	V	H	R	R	A	H	T
1715	AGG	AAT	GCC	AAT	CTG	GCG	GTG	CAC	CGG	CGT	GCC	CAC	ACT
	G	E	K	P	Y	G	C	Q	V	C	G	K	R
1754	GGC	GAG	AAG	CCA	TAT	GGG	TGC	CAG	GTG	TGC	GGG	AAG	CGG
	F	S	K	G	E	R	L	V	R	H	Q	R	I
1793	TTC	AGC	AAA	GGG	GAG	CGG	CTG	GTC	CGA	CAC	CAG	AGA	ATC
	H	T	G	E	K	P	Y	H	C	P	A	C	G
1832	CAT	ACA	GGG	GAG	AAG	CCC	TAC	CAC	TGT	CCT	GCC	TGC	GGG
	R	S	F	N	Q	R	S	I	L	N	R	H	Q
1871	CGA	AGC	TTC	AAC	CAG	AGG	TCC	ATC	CTC	AAC	CGG	CAC	CAG

FIG. 3

	K	T	Q	H	R	Q	E	P	L	V	Q	*
1910	AAG	ACC	CAG	CAC	CGC	CAG	GAG	CCG	CTG	GTG	CAG	TGA gca
1949	tag	cag	gtg	gca	ggc	agc	acc	atc	att	cat	ctt	cgg ata
1988	gca	ctg	gcg	acc	cta	gcg	ggc	gag	agg	ccc	ttc	agg gcc
2027	gcg	gcg	ggt	tga	gcg	cac	cat	cac	atc	taa	gcc	atc agc
2066	aag	ttt	gtt	ggt	ttt	aat	ctc	caa	aat	acg	tct	tga ttt
2105	tgt	ctg	act	ctt	tgc	cac	cac	cct	gat	cta	agc	cct tat
2144	cat	ctg	ctt	gaa	tca	cta	act	tgt	ctc	cac	ttg	cag ttt
2183	tta	aaa	gag	ttg	ctt	cca	ttt	gac	ttt	ttc	tgt	ctg ctg
2222	tac	caa	cat	atg	agt	ttc	agg	agg	ggt	cat	tga	tgc agt
2261	cat	tct	cag	tct	cct	cgg	agg	gag	tct	gaa	gat	gct taa
2300	aga	gca	tcc	aga	gat	ggc	gga	agc	tcc	tca	gca	gca gtt
2339	ggg	tat	tcc	tgt	ggt	gaa	act	gga	gaa	aga	gtt	gcc atg
2378	ggg	cag	agg	aag	gga	gga	ccc	tag	tcc	aga	gac	ttt tcg
2417	gct	gag	gtt	tcg	gca	gtt	ccg	cta	cca	gga	ggc	agc tgg
2456	acc	cca	gga	agc	tct	tag	ggg	gct	cca	gga	gct	ctg tcg
2495	tcg	gtg	gct	gag	gcc	cga	gtt	gca	cac	caa	gga	gca gat
2534	cct	gga	gct	gct	ggt	gct	gga	gca	gtt	cct	cac	tat cct
2573	gcc	ccg	cga	gtt	cta	cgc	ctg	gat	ccg	gga	gca	tgg ccc
2612	aga	gag	tgg	caa	ggc	cct	ggc	cgc	cat	ggt	gga	gga cct
2651	gac	aga	aag	agc	act	gga	ggc	caa	ggc	ggt	tcc	atg cca
2690	cag	gca	ggg	aga	gca	gga	gga	aac	agc	act	ttg	cag agg
2729	cgc	ttg	gga	gcc	agg	cat	cca	gct	ggg	gcc	agt	gga ggt
2768	taa	gcc	tga	atg	ggg	gat	gcc	ccc	tgg	gga	agg	agt tca
2807	agg	tcc	aga	ccc	agg	tac	cga	gga	gca	gct	cag	tca gga
2846	ccc	tgg	aga	tga	gac	acg	ggc	ctt	cca	gga	gca	agc act

FIG. 3

FIG. 3

3899 gca ccg cca gga gcc gct ggt gca gtg agc ata gca ggt

3938 ggc agg cag cac cat cat tca tct t

FIG. 3

0992181.08201

Structure of MDZ4 and alignment of SCAN box motifs

A

MDZ4 (389 a.a.)



B

SCAN box

	consensus	10	20	30	40	50	60
MDZ4	******
gi 11136033		1	PGPEAFRQRFQRYQE	---ASGPREALSRLRELC	HOWLRPEVHTKEQ	ILELLVLEQFLT	57
gi 6226799		42	httEiFRFRFRQCYQE	---SPGPREALQRLELCH	OWLRPEMHTKEQ	ILELLVLEQFLT	98
gi 3046745		36	SVWETSHLHFRLRYHE	---TSGQEALSRLRELC	HOWLRPEARTKAO	ILELLVLEQFLT	92
gi 3006231		35	PSPASHLRFRRFRFQE	---AAGPREALSRLRELC	HOWLRPEMRTKEQ	ILELLVLEQFLT	91
gi 1731420		47	RGPERSQRQRFGRYPE	---AAGPREALSRLRELC	HOWLRPEMRTKEQ	ILELLVLEQFLT	103
gi 11136100		49	PDPEIFRQRFRRFCYQ	---TFGPREALSRLRELC	HOWLRPEINTKEQ	ILELLVLEQFLT	105
gi 2978255		45	LQGEVFLRFRQRYQE	---TLGPREALIQURLCH	OWLRPEINTKEQ	ILELLVLEQFLT	101
		118	PGLEAARLRFRCFYED	---AIGQPEALAQURLCH	OWLRPEVHSKEQ	VLELLVLEQFLT	174

	Consensus	70	80	90
MDZ4	***
gi 11136033		58	ILPGEIQAWQVEHHPGSE	GEAVTILEDLERLDGPRQOV 96
gi 6226799		99	ILPEELQAWVRQHRPVS	GEEAVTILEDLERLDGPGQOV 137
gi 3046745		92	ILPGEIRTWQLHHPGSE	GEAVTILEDLERLDGPAIQV 131
gi 3006231		104	ILPQETQSRVQELHPS	GEEAVTIVEGMQRELGRLOOV 130
gi 1731420		106	ILPGLQSWVRQHPGSE	VEVVLLEYLRQLDEPAPQV 142
gi 11136100		100	ILPKELQWLQEYRPS	GEEAVTILEDLE--LDLSGQOV 142
gi 2978255		102	ILPGDLQAWVHEHYPS	GEEAVTILEDLERGTDEAVLQV 138
		175	ILPEELQTLVKDHLQ	ENGEEVVTILEDLERQIDILGRPV 140
			ALPPEIQAOVQVGWPG	SPPEAAALVDRLEWLDGPRKWV 213

FIG. 4

The MDZ4 gene (chr. 6p21.3-22.2)

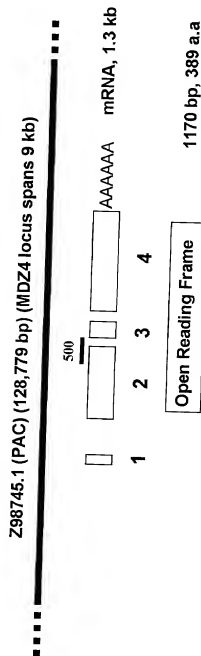


FIG. 5

MDZ4

nt: SEQ ID NO: 3027

aa: SEQ ID NO: 3029

1 gtt gtc aag gat tca gag cag atg tga tct gcg cta ggt
 40 ggc atc tcc tct cac gga tgc ctc gat ctc ggg gtt tcc
 79 aga aga aaa gat caa ggg aga att atc aag aat aga tta
 M A I T L
 118 ttt ttc tga ata gtt aaa cct ttg ATG GCC ATA ACC TTG
 T L Q T A E M Q E G L L A
 157 ACC CTT CAG ACT GCA GAG ATG CAG GAA GGA CTT CTG GCA
 V K V K E E E E E H S C G
 196 GTG AAG GTA AAG GAG GAA GAG GAG GAA CAT TCC TGT GGG
 P E S G L S R N N P H T R
 235 CCA GAA TCA GGC CTG TCA AGA AAT AAC CCT CAT ACC AGA
 E I F R R R F R Q F C Y Q
 274 GAG ATC TTT CGT AGA CGC TTC AGG CAG TTC TGC TAT CAG
 E S P G P R E A L Q R L Q
 313 GAG TCC CCT GGG CCC CGG GAG GCT CTT CAA AGA CTC CAG
 E L C H Q W L R P E M H T
 352 GAG CTC TGC CAT CAG TGG CTG AGA CCA GAG ATG CAC ACC
 K E Q I L E L L V L E Q F
 391 AAG GAG CAG ATC CTA GAG CTG CTG GTG CTG GAG CAG TTC
 L T I L P E E L Q A W V R
 430 CTG ACT ATC CTG CCT GAG GAG CTC CAG GCC TGG GTC AGA
 Q H R P V S G E E A V T V
 469 CAG CAC CGT CCT GTG AGT GGA GAG GAG GCA GTG ACT GTG
 L E D L E R E L D D P G E
 508 CTG GAG GAT TTG GAG AGA GAG CTG GAT GAC CCA GGA GAG

FIG. 6

0092161.080201

547 Q V L S H A H E Q E E F V
 CAG GTC CTG AGC CAT GCT CAT GAA CAG GAA GAG TTT GTA

586 K E K A T P G A A Q E S S
 AAG GAG AAG GCA ACT CCA GGA GCA GCT CAG GAG TCA TCA

625 N D Q F Q T L E E Q L G Y
 AAT GAC CAA TTC CAA ACC TTG GAA GAG CAG CTT GGG TAT

664 N L R E V C P V Q E I D G
 AAT TTG CGA GAG GTG TGC CCA GTT CAA GAG ATT GAT GGC

703 K A G T W N V E L A P K R
 AAG GCT GGG ACT TGG AAT GTG GAG TTA GCC CCA AAG AGG

742 E I S Q E V K S L I Q V L
 GAG ATT TCT CAG GAA GTG AAA TCT CTT ATA CAA GTT CTT

781 G K Q N G N I T Q I P E Y
 GGA AAA CAG AAT GGT AAT ATT ACT CAG ATT CCT GAG TAT

820 G D T C D R E G R L E K Q
 GGA GAT ACC TGT GAC CGT GAG GGC AGA TTG GAA AAG CAA

859 R V S S S V E R P Y I C S
 AGG GTG AGC TCT TCA GTG GAG AGA CCC TAT ATC TGT AGT

898 E C G K S F T Q N S I L I
 GAA TGT GGA AAA AGC TTC ACC CAG AAT TCC ATC CTT ATC

937 E H Q R T H T G E K P Y E
 GAG CAC CAG AGA ACA CAC ACA GGT GAG AAG CCT TAT GAA

976 C D E C G R A F S Q R S G
 TGT GAT GAG TGT GGG CGG GCC TTC AGC CAG AGG TCA GGC

1015 L F Q H Q R L H T G E K R
 CTA TTC CAG CAC CAG AGA CTC CAC ACT GGG GAG AAG CGC

1054 Y Q C S V C G K A F S Q N
 TAC CAG TGC AGT GTT TGT GGC AAA GCC TTC AGC CAG AAT

1093 A G L F H H L R I H T G E
 GCC GGG CTT TTC CAT CAC CTC AGA ATT CAC ACT GGG GAG

FIG. 6

0322161.032201

102089*1912660

Structure of MDZ7

MDZ7 (248 a.a.)

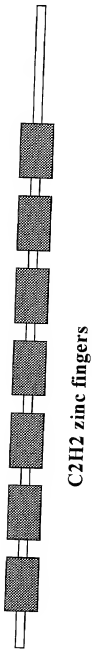


FIG. 7

102090" 10122660

MDZ7 gene (chr. 16p11.2)

AC002310.1 (BAC) (120,955 bp) (MDZ7 locus spans 5.5 kb)

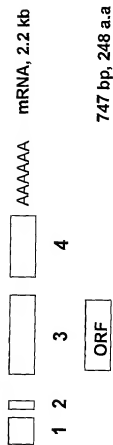


FIG. 8

MDZ7

nt: SEQ ID NO: 4407

aa: SEQ ID NO: 4409

1 cc tgt tcc cgc tgc ccc tgc ggc tgg cac tgc cag gag
 39 tac tca gag ctc aaa gct ggg atc tgc agt ccc tta ccc
 78 act cag tgc acg ccg cct aag gct ttg cgc ttc acc ttt
 117 act cac ctc gaa gcc ctg gac atc cgc atc tgc cct aag
 156 act tct cac ctc agt agc aga agg aag tgc cgt cag ctg
 195 gcc aca gcc tct ctc cta gga gac cgt ccg gga aaa gcg
 234 agt cag ggt aga ccc tga ggc ccc tca gct ccg gct att
 273 ttc aga tct gtc gct cct tca ccc tca gcc ttt caa aca
 312 ggc cac tcc aaa aaa aag ccc aat cac agc ctt cct tct
 351 tct cct ggc ctt ccg gca ctg tcc aat caa cgt acg cca
 390 tct atc gga ttt tca gtt ccc aaa ccc gct ttt atc tgc
 429 tgg gtg gaa gga gaa gtg gag gcg tgg agc ccg gag gcc
 468 cag gat ccc gac ggt gag agc tct gca gct ttc agc agg
 507 ggc caa gga cag gaa gca gga tcc agg gat ggg aat gag
 546 aag aag gaa agg ctg aag aag tgt cca aaa caa aaa gag
 585 gtg gcg cat gaa gtg gct gtc aag gag tgg tgg ccc agc
 624 gtc gcc tgc cca gag ttc tgc aac cct agg cag agc ccc
 663 M N P W L K D T L T R R L
 ATG AAT CCC TGG CTC AAG GAC ACT CTG ACC CGA AGA CTG
 703 P H S C P D C G R N F S Y
 CCC CAC TCT TGC CCA GAC TGT GGC CGC AAC TTC AGC TAC
 742 P S L L A S H Q R V H S G
 CCT TCC CTC CTG GCC AGC CAC CAG CGG GTC CAC TCC GGG

FIG. 9

E R P F S C G Q C Q A R F
 781 GAG CGG CCC TTC TCC TGC GGC CAG TGT CAG GCG CGT TTC

 S Q R R Y L L Q H Q F I H
 820 TCC CAG CGC AGG TAC CTG CTC CAG CAT CAG TTC ATC CAC

 T G E K P Y P C P D C G R
 859 ACC GGC GAG AAG CCC TAC CCC TGC CCC GAC TGC GGG CGC

 R F R Q R G S L A I H R R
 898 CGC TTC CGC CAG AGG GGT TCC CTG GCT ATC CAC AGG CGG

 A H T G E K P Y A C S D C
 937 GCT CAC ACC GGG GAG AAG CCT TAC GCG TGC TCA GAC TGC

 K S R F T Y P Y L L A I H
 976 AAG AGT CGC TTC ACT TAC CCC TAC CTG CTG GCC ATC CAC

 Q R K H T G E K P Y S C P
 1015 CAG CGC AAG CAC ACG GGC GAG AAG CCC TAC AGC TGC CCC

 D C S L R F A Y T S L L A
 1054 GAT TGC AGC CTC CGT TTC GCC TAC ACC TCC CTG CTG GCC

 I H R R I H T G E K P Y P
 1093 ATC CAC AGG CGC ATA CAC ACC GGC GAG AAG CCC TAC CCC

 C P D C G R R F T Y S S L
 1132 TGT CCT GAC TGC GGC CGC CGC TTC ACC TAT TCT TCC CTC

 L L S H R R I H S D S R P
 1171 CTC CTC AGT CAC CGG CGC ATT CAC TCC GAC AGC CGG CCC

 F P C V E C G K G F K R K
 1210 TTC CCC TGC GTG GAG TGT GGG AAA GGC TTC AAG CGC AAG

 T A L E A H R W I H R S C
 1249 ACC GCC CTG GAA GCC CAT CGG TGG ATC CAC CGC TCC TGC

 S E R R A W Q Q A V V G R
 1288 AGC GAG AGG CGC GCG TGG CAG CAG GCC GTG GTG GGG CGT

 S E P I P V L G G K D P P
 1327 TCA GAG CCC ATC CCT GTT TTG GGA GGC AAG GAT CCC CCA

 V H F R H F P D I F Q E C
 1366 GTT CAC TTC CGG CAC TTT CCA GAT ATA TTT CAA GAG TGT

 G *
 1405 GGG TGA tgg cgt tca cac aaa ctg gtc agc gtt tcc ctg

FIG. 9

1443 gag agg aag agg caa gat att tgc atg ttc cct gga ttt
 1482 tgt att ttt tga taa aga tat att ctt ggg cca cag tag
 1521 ctg gag ata taa tgc cgg agg att ctt ttt ttt ttt
 1560 ttg aga cag agt ctg tct cta ttg cct ggg ctg gag tgc
 1599 agt ggc cca agc tac gct cac tgc aag ctc cac ctc ctg
 1638 ggt tca cac cat tct cct gct tca gtc tcc cga gta gct
 1677 gga att aca agc acc cgc cac cac gcc caa cta ata ttt
 1716 tgt att ttt agt aga gac ggg ggt ttc acc gtg tta gcc
 1755 agg atg gtc tgc atc tcc tga ctt cgt gat cct ccc gcc
 1794 tgc gcc tcc caa agt gct ggg att aca ggc gtg agc cac
 1833 tgc acc cag cct ctt ttt ttt ttt gag atg gag ttt cgc
 1872 tct tgt tgc cca ggc tag agt gca atg gca tga tct tgg
 1911 ctc act gca acc tcc gcc tcc tag gtt caa gcg att ctc
 1950 ctg ccc cag cct ctt gag tag ctg gga tta cag gca ccc
 1989 acg acc atg cct ggc taa ttg cat ttt tac tag aga cag
 2028 gtt tca cca tgt tgg cca ggc tgg tct cca att cct gac
 2067 ctc agg tga tcc acc cga ctt ggc ctc cca aag ttc tgg
 2106 gat tac att ttt ttt tta aag aaa gaa taa att aat tgt
 2145 gat taa agt tga aat caa ggc ata gtt aaa aaa aaa aaa
 2184 aaa aaa aaa aaa aaa nnc ctg ttc ccg ctg ccc ctc ggg
 2223 ctg gca ctg cca gga gta ctc aga gct caa agc tgg gat
 2262 ctg cag tcc ctt acc cac tca gtg cac gcc gcc taa ggc
 2301 ttt gcg ctt cac ctt tac tca cct cga agc cct gga cat
 2340 ccg cat ctg ccc taa gac ttc tca cct cag tag cag aag
 2379 gaa gtc gcg tca gct ggc cac agc ctc tct cct agg aga
 2418 ccg tcc ggg aaa agc gag tca ggg tag acc ctg agg ccc

FIG. 9

00022181.00001

2457 ctc agc tcc ggc tat ttt cag atc tgt cgc tcc ttc acc
 2496 ctc agc ctt tca aac agg cca ctc caa aaa aaa gcc caa
 2535 tca cag cct tcc ttc ttc tcc tgg cct tcc ggc act gtc
 2574 caa tca acg tac gcc atc tat cgg att ttc agt tcc caa
 2613 acc cgc ttt tat ctc gtg ggt gga agg aga agt gga ggc
 2652 gtg gag ccc gga ggc cca gga tcc cga cgg tga gag ctc
 2691 tgc agc ttt cag cag ggg cca agg aca gga agc agg atc
 2730 cag gga tgg gaa tga gaa gaa gga aag gct gaa gaa gtg
 2769 tcc aaa aca aaa aga ggt ggc gca tga agt ggc tgt caa
 2808 gga gtg gtg gcc cag cgt cgc ctg ccc aga gtt ctg caa
 2847 ccc tag gca gag ccc cat gaa tcc ctg gct caa gga cac
 2886 tct gac ccg aag act gcc cca ctc ttg ccc aga ctg tgg
 2925 ccg caa ctt cag cta ccc ttc cct cct ggc cag cca cca
 2964 gcg ggt cca ctc cgg gga gcg gcc ctt ctc ctg cgg cca
 3003 gtg tca ggc gcg ttt ctc cca gcg cag gta cct gct cca
 3042 gca tca gtt cat cca cac cgg cga gaa gcc cta ccc ctg
 3081 ccc cga ctg cgg gcg ccg ctt ccg cca gag ggg ttc cct
 3120 ggc tat cca cag gcg ggc tca cac cgg gga gaa gcc tta
 3159 cgc gtg ctc aga ctg caa gag tcg ctt cac tta ccc cta
 3198 cct gct ggc cat cca cca gcg caa gca cac ggg cga gaa
 3237 gcc cta cag ctg ccc cga ttg cag cct ccg ttt cgc cta
 3276 cac ctc cct gct ggc cat cca cag gcg cat aca cac cgg
 3315 cga gaa gcc cta ccc ctg tcc tga ctg cgg ccg ccg ctt
 3354 cac cta ttc ttc cct cct cct cag tca ccg gcg cat tca
 3393 ctc cga cag ccg gcc ctt ccc ctg cgt gga gtg tgg gaa
 3432 agg ctt caa gcg caa gac cgc cct gga agc cca tcg gtg

FIG. 9

0991191

1992

Structure of MDZ12 and alignment of KRAB motifs

A

MDZ12a (483 a.a.)



KRAB motif

C2H2 zinc fingers

MDZ12bL (332 a.a.)



C2H2 zinc fingers

B

KRAB motif

consensus	1	VTEDVAVYFSQEWEQLDPAQKNLY-RDVMLENSNVLSLG-EKVPKPDLLISOLEQGEPPW	61
MDZ12	1	-----mwlgtsgksqglpghclenplqechpqaclaeewalkGISRPSVISQPEQKEEPW	53
gi 12643434	28	VTFKDVIVDFTQEEWKQLDPGQDLF-RDVTLENTYHLVSIQ-LQVSKPDVISOLEQGTETLW	88
gi 141686	1	-----DFTQEEWGQLDPTQRILY-RDVMLENTFYLLSIG-PELPKPEVISOLEQGTETLW	53
gi 549835	14	VTFKDVFVDFTRFEWKLLDTAQIVY-RNVMLENTYKLVLSLG-YQITKPDVILRLKEGEEPPW	74
gi 3445181	20	VTFGDVAVDFSQEWEWLNPIQRNLY-RKVMLENTYKLVLSLG-LCVSKPDVILSSLEQGEKPT	80
gi 141685	4	VTFGDVAVHFSREWEKQLDPGQALY-RVMLENTYKLVLSLG-YEVKMPDVIKLEEGEPPW	65
gi 1731444	8	FSFDLSVDFTRQEWQLLDPGQKNLY-KDVMLENTYKLVLSLG-YEVKMPDVIKLEEGEPPW	68
gi 6137309	237	VTFKDVAVCFSDQWSDLDPTQKEFYqYVLEEDCGIVVSLSF-PIPRDEISQV-REEEPW	297
gi 3511122	1	MAEDVAVYFSQEWEGLDPAQALY-RRVMLDNFALVASLG1-STSRPRVVIQLERGEPPW	61

FIG. 10

102080"18122660

Splice Variants of the hMDZ12 Zinc Finger Gene

AC018946 (BAC, 173 kb)

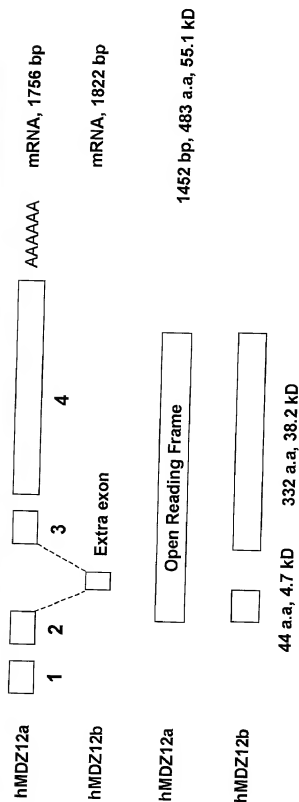


FIG. 11

MDZ12a

nt: SEQ ID NO: 5770

aa: SEQ ID NO: 5772

1 gaa tcc cgg tcg ggt tct ggg agg cac cgc ctc ggg gtt
 40 gcg gcc cgg gtg cgg ctc gcc ggt gga gga ctc act tcc
 79 tgc tcc atc ccc gcc tgg gcc ctg ggg cgg aac tga tga
 118 cgc ttg ata M W L G T S G K S G
 ATG TGG CTG GGG ACT TCA GGG AAG AGT GGG
 157 L P G H C L E N P L Q E C
 TTA CCT GGA CAC TGC TTA GAG AAT CCT CTC CAG GAA TGC
 196 H P A Q L E E W A L K G I
 CAC CCA GCA CAG TTA GAA GAA TGG GCT CTC AAA GGA ATT
 235 S R P S V I S Q P E Q K E
 TCC AGG CCT AGT GTA ATC TCC CAG CCG GAG CAG AAA GAA
 274 E P W V L P L Q N F E A R
 GAG CCA TGG GTC CTA CCA CTC CAA AAC TTT GAG GCG AGG
 313 K I P R E S H T D C E H Q
 AAG ATC CCG AGG GAA AGC CAC ACA GAC TGT GAG CAT CAG
 352 V A K L N Q D N S E T A E
 GTG GCA AAG CTC AAT CAG GAC AAT TCT GAA ACA GCA GAA
 391 Q C G T S S E R T N K D L
 CAA TGT GGA ACA TCC TCA GAA AGG ACC AAT AAA GAT CTT
 430 S H T L S W G G N W E Q G
 TCT CAT ACT CTT AGT TGG GGA GGA AAC TGG GAG CAA GGC
 469 L E L E G Q H G T L P G E
 CTA GAA TTA GAA GGG CAA CAT GGA ACC CTT CCA GGA GAG
 508 G Q L E S F S Q E R D L N
 GGC CAG CTG GAG TCC TTT TCA CAG GAG AGG GAT TTA AAC
 547 K L L D G Y V G E K P M C
 AAG CTC CTG GAT GGA TAT GTA GGA GAG AAG CCT ATG TGT

FIG. 12

09922181-080201

586 A E C G K S F N Q S S Y L
 GCA GAA TGC GGG AAA AGC TTT AAC CAG AGT TCC TAT CTC

625 I R H L R T H T G E R P Y
 ATA AGA CAC CTA AGA ACC CAC ACT GGC GAG AGG CCC TAT

664 T C I E C G K G F K Q S S
 ACG TGC ATT GAG TGT GGG AAA GGC TTC AAA CAG AGC TCA

703 D L V T H R R T H T G E K
 GAC CTT GTC ACC CAT CGC AGA ACA CAC ACA GGA GAG AAG

742 P Y Q C K G C E K K F S D
 CCC TAC CAA TGC AAG GGG TGT GAG AAG AAA TTC AGC GAC

781 S S T L I K H Q R T H T G
 AGC TCA ACA CTC ATC AAA CAT CAG AGA ACC CAC ACA GGG

820 E R P Y E C P E C G K T F
 GAG AGA CCC TAT GAG TGC CCA GAG TGT GGA AAG ACT TTT

859 G R K P H L I M H Q R T H
 GGG CGG AAG CCA CAC CTC ATA ATG CAC CAA AGA ACC CAC

898 T G E K P Y A C L E C H K
 ACA GGC GAG AAG CCC TAC GCG TGC CTG GAA TGT CAC AAA

937 S F S R S S N F I T H Q R
 AGC TTC AGT CGA AGC TCA AAT TTC ATC ACT CAC CAG AGG

976 T H T G V K P Y R C N D C
 ACC CAC ACA GGG GTG AAG CCT TAC AGG TGT AAT GAC TGT

1015 G E S F S Q S S D L I K H
 GGG GAG AGT TTT AGC CAG AGC TCG GAT TTG ATT AAG CAC

1054 Q R T H T G E R P F K C P
 CAA CGA ACC CAC ACG GGA GAA CGG CCC TTC AAA TGC CCG

1093 E C G K G F R D S S H F V
 GAG TGC GGG AAG GGC TTC AGA GAT AGT TCT CAT TTT GTA

1132 A H M S T H S G E R P F S
 GCT CAC ATG AGC ACT CAT TCA GGA GAG AGG CCT TTC AGT

1171 C P D C H K S F S Q S S H
 TGT CCT GAC TGC CAC AAA AGC TTC AGT CAG AGC TCA CAT

1210 L V T H Q R T H T G E R P
 TTG GTC ACG CAC CAA AGA ACA CAC ACA GGT GAG AGA CCT

FIG. 12

0992131-080201

1249 F K C E N C G K G F A D S
 TTT AAG TGC GAA AAC TGT GGG AAA GGA TTC GCC GAC AGC

1288 S A L I K H Q R I H T G E
 TCC GCC CTC ATT AAG CAC CAA CGA ATC CAC ACC GGA GAA

1327 R P Y K C G E C G K S F N
 AGA CCC TAC AAA TGT GGA GAG TGT GGG AAG AGC TTC AAT

1366 Q S S H F I T H Q R I H L
 CAG AGC TCC CAC TTT ATT ACC CAT CAG CGA ATC CAC TTA

1405 G D R P Y R C P E C G K T
 GGA GAC AGG CCC TAT CGA TGT CCT GAG TGT GGC AAG ACC

1444 F N Q R S H F L T H Q R T
 TTC AAT CAG CGT TCC CAT TTC CTC ACA CAC CAG AGA ACG

1483 H T G E K P F H C S K C N
 CAT ACA GGA GAA AAA CCT TTC CAC TGT AGT AAA TGT AAC

1522 K S F R Q K A H L L C H Q
 AAG AGC TTC CGT CAG AAA GCG CAT CTT TTA TGC CAT CAA

1561 N T H L I *
 AAC ACC CAT TTG ATT TAG gaa gta gtc ttt ggt gtt cag

1600 ctg ctc cct tgc aca ttt tca ttg cta ctg tct tca agc

1639 acc cca aat aga gaa aac ctg ggc gtc agt ggc tca att

1678 tgg gcc ctg atc tat tct ccc tct ttc ttg tct atg tta

1717 taa cag aga gga taa act taa agg gtc caa ata acg gtc

1756 caa aaa aaa aaa aaa aaa aaa a

FIG. 12

MDZ12b

nt: SEQ ID NO: 6938
 aa: SEQ ID NO: 6939 and 6940

M	W	L	G	T	S	G	K	S	G	L	P	G	13
ATG	TGG	CTG	GGG	ACT	TCA	GGG	AAG	AGT	GGG	TTA	CCT	GGA	39
H	C	L	E	N	P	L	Q	E	C	H	P	A	26
CAC	TGC	TTA	GAG	AAT	CCT	CTC	CAG	GAA	TGC	CAC	CCA	GCA	78
Q	L	E	E	W	A	L	K	G	L	G	W	T	39
CAG	TTA	GAA	GAA	TGG	GCT	CTC	AAA	GGA	CTG	GGT	TGG	ACT	117
L	T	S	A	T	*								45
CTC	ACC	TCT	GCC	ACT	TAA	c	t	t	c	t	c	t	162
aaa	agg	aga	aatt	tcc	agg	cct	agt	gta	atc	ccc	agc	cgga	214
agc	cat	ggg	tcc	tacc	act	ccaaa	ctt	ttag	ggc	gagga	aagat	ccc	266
aag	ccac	acag	act	gtg	agc	atc	aggt	ggc	aaag	ctca	atc	agg	318
gaa	acag	caga	aca	atg	tgg	aac	atc	ctc	caga	aagg	acca	ataa	370
ctc	ata	ctc	tct	agt	tggg	gagg	aaact	ggg	agca	aagg	cc	taga	422
gca	acat	gga	acc	ctt	cc	cagg	agag	ggcc	agct	ggag	ctc	tttt	474
aggg	attta	aaaca	agct	cct	ggat	ggat	atg	tagg	agaga	aagc	ctATG	TGT	525
A	E	C	G	K	S	F	N	Q	S	S	Y	L	15
GCA	GAA	TGC	GGG	AAA	AGC	TTT	AAC	CAG	AGT	TCC	TAT	CTC	564
I	R	H	L	R	T	H	T	G	E	R	P	Y	28
ATA	AGA	CAC	CTA	AGA	ACC	CAC	ACT	GGC	GAG	AGG	CCC	TAT	603
T	C	I	E	C	G	K	G	F	K	Q	S	S	41
ACG	TGC	ATT	GAG	TGT	GGG	AAA	GGC	TTC	AAA	CAG	AGC	TCA	642
D	L	V	T	H	R	R	T	H	T	G	E	K	54
GAC	CTT	GTC	ACC	CAT	CGC	AGA	ACA	CAC	ACA	GGA	GAG	AAG	681
P	Y	Q	C	K	G	C	E	K	K	F	S	D	67
CCC	TAC	CAA	TGC	AAG	GGG	TGT	GAG	AAG	AAA	TTC	AGC	GAC	720

FIG. 13

S	S	T	L	I	K	H	Q	R	T	H	T	G	80
AGC	TCA	ACA	CTC	ATC	AAA	CAT	CAG	AGA	ACC	CAC	ACA	GGG	759
E	R	P	Y	E	C	P	E	C	G	K	T	F	93
GAG	AGA	CCC	TAT	GAG	TGC	CCA	GAG	TGT	GGA	AAG	ACT	TTT	798
G	R	K	P	H	L	I	M	H	Q	R	T	H	106
GGG	CGG	AAG	CCA	CAC	CTC	ATA	ATG	CAC	CAA	AGA	ACC	CAC	837
T	G	E	K	P	Y	A	C	L	E	C	H	K	119
ACA	GGC	GAG	AAG	CCC	TAC	GCG	TGC	CTG	GAA	TGT	CAC	AAA	876
S	F	S	R	S	S	N	F	I	T	H	Q	R	132
AGC	TTC	AGT	CGA	AGC	TCA	AAT	TTC	ATC	ACT	CAC	CAG	AGG	915
T	H	T	G	V	K	P	Y	R	C	N	D	C	145
ACC	CAC	ACA	GGG	GTG	AAG	CCT	TAC	AGG	TGT	AAT	GAC	TGT	954
G	E	S	F	S	Q	S	S	D	L	I	K	H	158
GGG	GAG	AGT	TTT	AGC	CAG	AGC	TCG	GAT	TTG	ATT	AAG	CAC	993
Q	R	T	H	T	G	E	R	P	F	K	C	P	171
CAA	CGA	ACC	CAC	ACG	GGA	GAA	CGG	CCC	TTC	AAA	TGC	CCG	1032
E	C	G	K	G	F	R	D	S	S	H	F	V	184
GAG	TGC	GGG	AAG	GGC	TTC	AGA	GAT	AGT	TCT	CAT	TTT	GTA	1071
A	H	M	S	T	H	S	G	E	R	P	F	S	197
GCT	CAC	ATG	AGC	ACT	CAT	TCA	GGA	GAG	AGG	CCT	TTC	AGT	1110
C	P	D	C	H	K	S	F	S	Q	S	S	H	210
TGT	CCT	GAC	TGC	CAC	AAA	AGC	TTC	AGT	CAG	AGC	TCA	CAT	1149
L	V	T	H	Q	R	T	H	T	G	E	R	P	223
TTG	GTC	ACG	CAC	CAA	AGA	ACA	CAC	ACA	GGT	GAG	AGA	CCT	1188
F	K	C	E	N	C	G	K	G	F	A	D	S	236
TTT	AAG	TGC	GAA	AAC	TGT	GGG	AAA	GGA	TTC	GCC	GAC	AGC	1227
S	A	L	I	K	H	Q	R	I	H	T	G	E	249
TCC	GCC	CTC	ATT	AAG	CAC	CAA	CGA	ATC	CAC	ACC	GGA	GAA	1266
R	P	Y	K	C	G	E	C	G	K	S	F	N	262
AGA	CCC	TAC	AAA	TGT	GGA	GAG	TGT	GGG	AAG	AGC	TTC	AAT	1305
Q	S	S	H	F	I	T	H	Q	R	I	H	L	275
CAG	AGC	TCC	CAC	TTT	ATT	ACC	CAT	CAG	CGA	ATC	CAC	TTA	1344
G	D	R	P	Y	R	C	P	E	C	G	K	T	288
GGA	GAC	AGG	CCC	TAT	CGA	TGT	CCT	GAG	TGT	GGC	AAG	ACC	1383

FIG. 13

102080-18122600

F	N	Q	R	S	H	F	L	T	H	Q	R	T	301
TTC	AAT	CAG	CGT	TCC	CAT	TTC	CTC	ACA	CAC	CAG	AGA	ACG	1422
H	T	G	E	K	P	F	H	C	S	K	C	N	314
CAT	ACA	GGA	GAA	AAA	CCT	TTC	CAC	TGT	AGT	AAA	TGT	AAC	1461
K	S	F	R	Q	K	A	H	L	L	C	H	Q	327
AAG	AGC	TTC	CGT	CAG	AAA	GCG	CAT	CTT	TTA	TGC	CAT	CAA	1500
N	T	H	L	I	*								323
AAC	ACC	CAT	TTG	ATT	TAG								1518

FIG. 13

102090*18122660

102020" T8T22660

MDZ3 Expression: RT-PCR Analysis

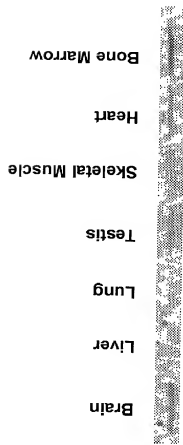


FIG. 14

MDZ7 Expression: RT-PCR Analysis

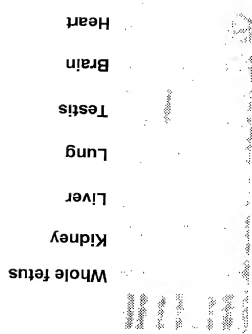


FIG. 15

102090*18122650

Expression of MDZ12 in human tissues

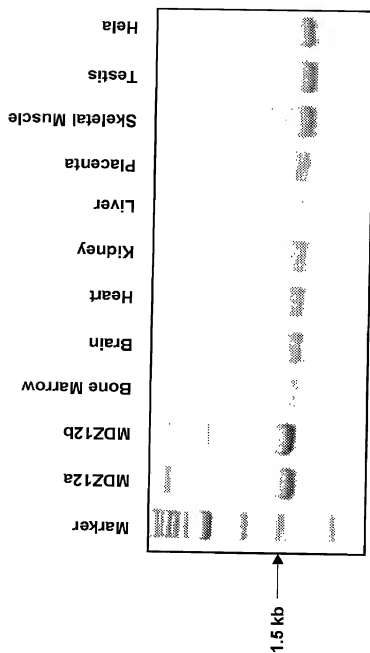


FIG. 16